

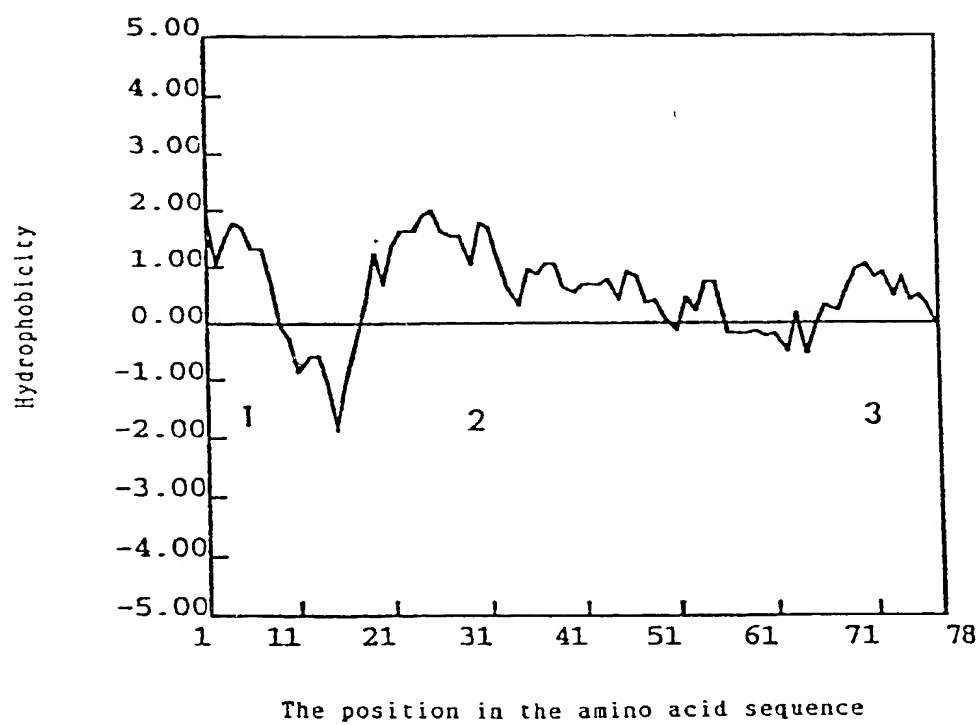
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5'		10		19		28		37		46		55						
	GTG	GCC	ATG	CTG	GCC	AAC	GCC	CTG	GTC	TGT	CAT	GTC	ATC	TTC	AAG	AAC	CAG	CGA
									Val	Cys	His	Val	Ile	Phe	Lys	Asn	Gln	Arg
		64		73		82		91		100		109						
	ATG	CAC	TCG	GCC	ACC	AGC	CTC	TTC	ATC	GTC	AAC	CTG	GCA	GTT	GCC	GAC	ATA	ATG
	Met	His	Ser	Ala	Thr	Ser	Leu	Phe	Ile	Val	Asn	Leu	Ala	Val	Ala	Asp	Ile	Met
		118		127		136		145		154		163						
	ATC	ACG	CTG	CTC	AAC	ACC	CCC	TTC	ACT	TTG	GTT	CGC	TTT	GTC	AAC	AGC	ACA	TGG
	Ile	Thr	Leu	Leu	Asn	Thr	Pro	Phe	Thr	Leu	Val	Arg	Phe	Val	Asn	Ser	Thr	Trp
		172		181		190		199		208		217						
	ATA	TTT	GGG	AAG	GCC	ATG	TOC	CAT	GTC	AGC	CGC	TTT	GCC	CAG	TAC	TGC	TCA	CTG
	Ile	Phe	Gly	Lys	Gly	Met	Cys	His	Val	Ser	Arg	Phe	Ala	Gln	Tyr	Cys	Ser	Leu
		226		235														
	CAC	GTC	TCA	GCA	CTG	ACA	3'											
	His	Val	Ser	Ala	Leu	Thr												

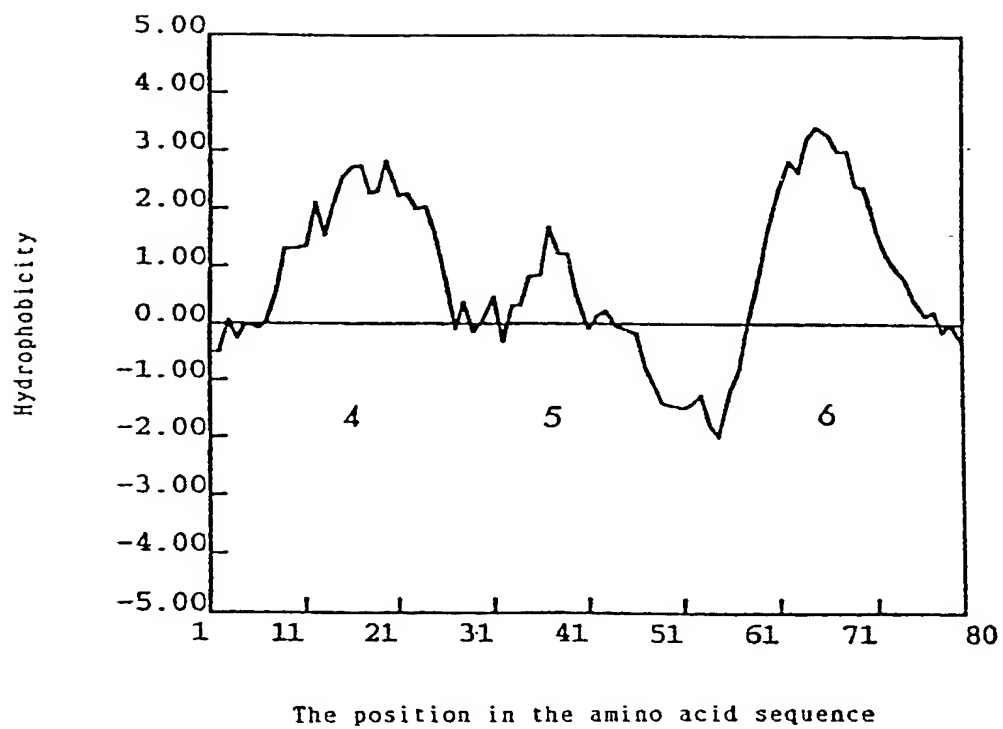
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		9		18		27		36		45		54						
5'	GAG	CCA	GCT	GAC	CTC	TTC	TGG	AAG	AAC	CTG	GAC	TTC	CCC	ACC	TTC	ATC	CTG	CTC
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Glu	Pro	Ala	Asp	Leu	Phe	Trp	Lys	Asn	Leu	Asp	Leu	Pro	Thr	Phe	Ile	Leu	Leu
			63		72		81		90		99		108					
	AAC	ATC	CTG	CCC	CTC	CTC	ATC	ATC	TCT	GTG	GCC	TAC	GTT	CGT	GTG	ACC	AAG	AAA
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Asn	Ile	Leu	Pro	Leu	Leu	Ile	Ile	Ser	Val	Ala	Tyr	Val	Arg	Val	Thr	Lys	Lys
			117		126		135		144		153		162					
	CTG	TGG	CTG	TGT	AAT	ATG	ATT	GTC	GAT	GTG	ACC	ACA	GAG	CAG	TAC	TTT	GCC	CTG
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Leu	Trp	Leu	Cys	Asn	Met	Ile	Val	Asp	Val	Thr	Thr	Glu	Gln	Tyr	Phe	Ala	Leu
			171		180		189		198		207		216					
	CGG	CCC	AAA	AAG	AAG	AAG	ACC	ATC	AAG	ATG	TTC	ATG	CTG	GTG	GTA	GTC	CTC	TTT
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	Arg	Pro	Lys	Lys	Lys	Lys	Thr	Ile	Lys	Met	Leu	Met	Leu	Val	Val	Val	Leu	Phe
			225		234													
	GCC	CTC	TGC	TGG	TTC	CTC	GAC	3'										
	---	---	---	---	---	---	---	---										
	Ala	Leu	Cys	Trp	Leu	Pro	Leu	Asp										

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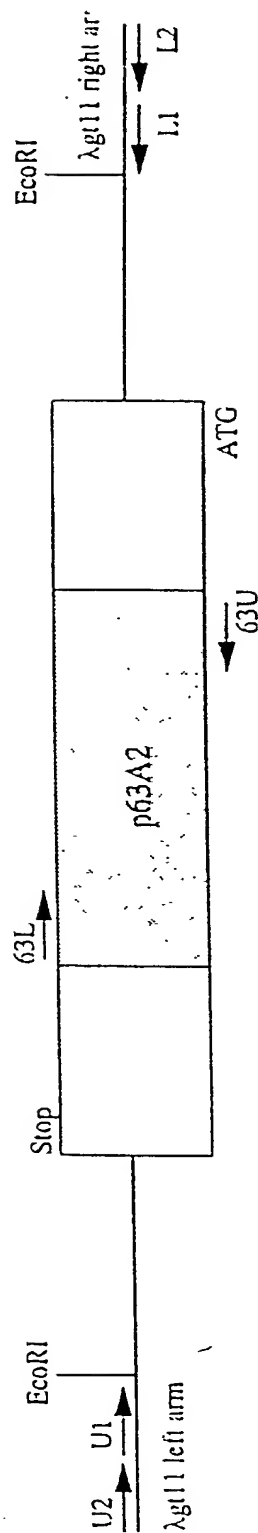
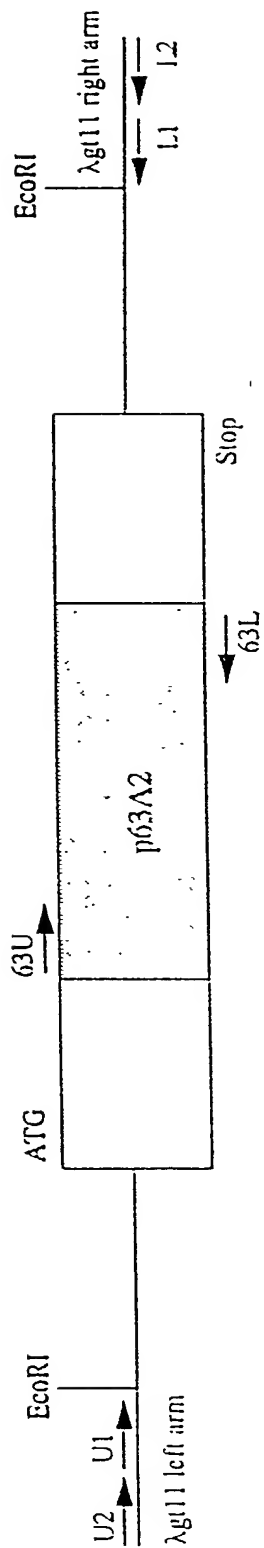
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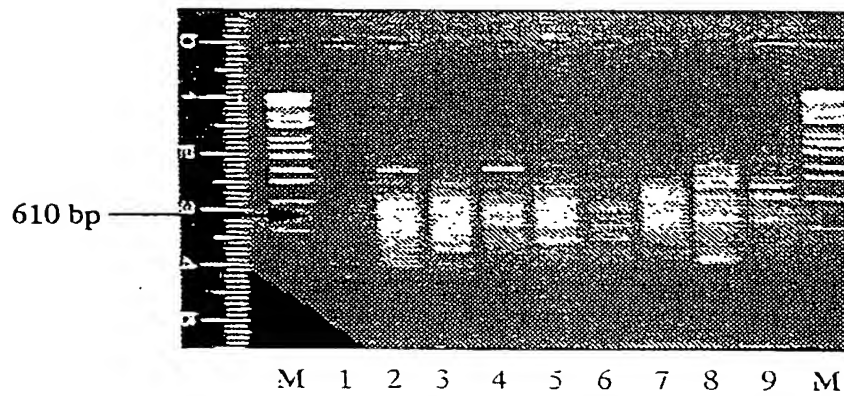
p63A2		10	20	30	40	50	
P30731	1	VCHVLEKQOR	MHSATSLFIV	NLAVADIMIT	LLNTPFTLVR	EVNSTWIFGK	50
	1	VCHVLEKQOR	MHSATSLFIV	NLAVADIMIT	LLNTPFTLVR	EVNSTWIFGK	50
p63A2		60	70	80	90	100	
P30731	51	GMCHVSRFAQ	YCSLHVSALT				100
	51	GMCHVSRFAQ	YCSLHVSALT	LTALAVIDRHQ	VIMHPLKPRI	SITKGVITYLA	100
p63A2		110	120	130	140	150	
P30731	101				EE	ADLEWKNLDL	150
	101	VIWMATFFS	LPHAICQKLF	TFKYSEDIVR	SLCLPDPFPH	ADLEWKYLDL	150
p63A2		160	170	180	190	200	
P30731	151	PTFILLNIEP	LLITSVAYVR	VTKKLWLCNM	IVDVTEQYF	ALRPKGGKTI	200
	151	ATFILLYLLP	LFITSVAYAR	VAKKLWLCNT	IGDVTEQYF	ALRRKGGKTV	200
p63A2		210	220	230	240	250	
P30731	201	KHMLVWVL	250
	201	KHMLVWVL	250

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M: λ DNA/Sty I marker

lane 1; 63U~63L

lane 2: U1~63U

lane 3; U1~63L

lane 4: U2~63U

lane 5; U2~63L

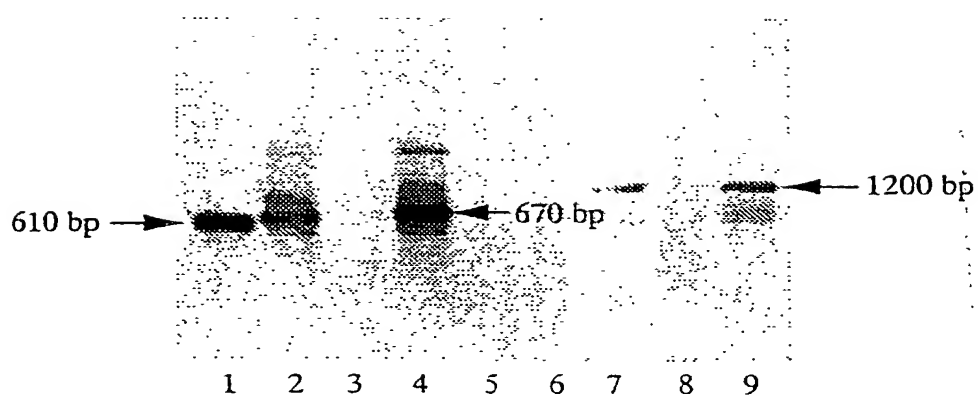
lane 6: L1~63U

lane 7: L1~63L

lane 8; L2~63U

lane 9; L2~63L

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lane 1 ; 63U~63L
lane 2 ; U1~63U
lane 3 ; U1~63L
lane 4 ; U2~63U
lane 5 ; U2~63L
lane 6 ; L1~63U
lane 7 ; L1~63L
lane 8 ; L2~63U
lane 9 ; L2~63L


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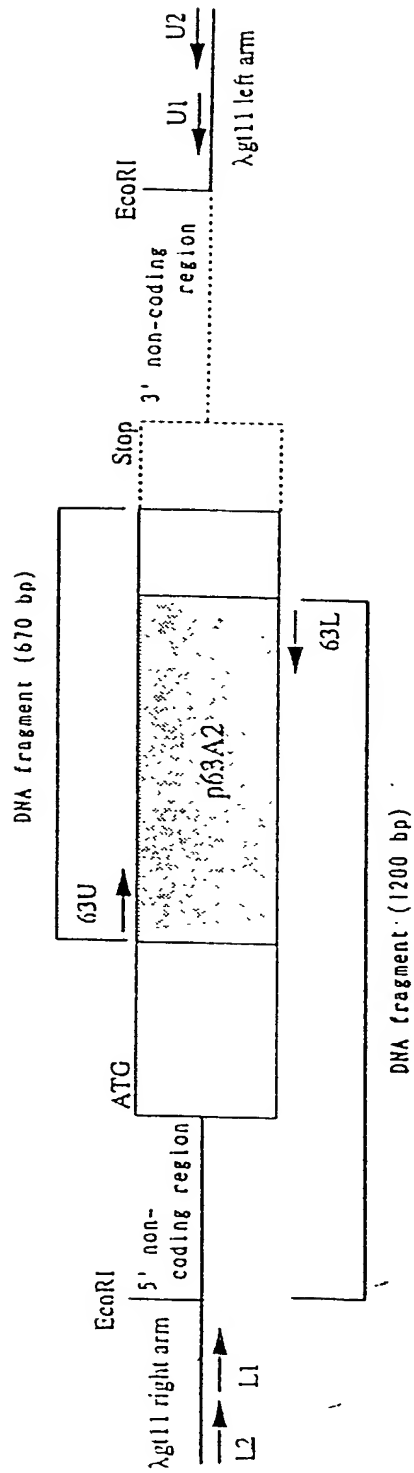
63A2-5'. SEQ      10      20      30      40      50
GGGCCCCCTTACACCTTTGTGATTGATCCGGGGTTTC-AAGGGTGCATGATGAAAG
MUSGIR.DNA      130      140      150      160      170      180
GGGCTTCCTCTGTGCCCCCGTCCCTGCTCCCAAGGCTCCCTCTGTGGTGTGACTCCTC
63A2-5'. SEQ      60      70      80      90      100      110
GAGTAAAGCCACATGAGCAGGGCTTCAACCCTGGGGTTCTGGGACTCAGCGCCCTAGTGC
MUSGIR.DNA      130      140      150      160      170      180
TAGCCCGGTGCGCTCAGC--CCCTGCACAC-CAGCCTCCAGGCACAGAGCCCGCAGGGA
63A2-5'. SEQ      120      130      140      150      160      170
TTCCTGCCACAAAGTTCTCCCAAGGGAGGGGTGGCTCCTGCATAATGATCCTCAACCTC
MUSGIR.DNA      190      200      210      220      230      240
GCTCAGCCC-----TTGTGCTTAGAGCTGCAAGTGGCT-GGACATGAAGTTCTCCTGTC
63A2-5'. SEQ      180      190      200      210      220      230
TTGCTGCTCTGTCTCTCCTCCCTTGGTGGAGGCCACCGAGGCCACGAGGGCGGCGGAC
MUSGIR.DNA      300      310      320      330      340      350
CTGCTTCTCTTCTCTCTGTCTGCTCAGTGGAGCTACTGAGCAACCGCAGGTGCTCACTGAG
63A2-5'. SEQ      240      250      260      270      280      290
GAGCAGAGCGCGGAGGGCGGCTGGCCATGCCAAATGCCCTGCACACTTCTTCTTGGAAC
MUSGIR.DNA      360      370      380      390      400      410
CATCCAGCATGAGGAGCGCCCTGACCGGGCCCAACGCCCTCCTCGCACTTC--TGGGCC
63A2-5'. SEQ      300      310      320      330      340      350
AACTACACCTTCTCGCACTGGCAGAACTTTGTGGCAGGAGGTGCTACGCGCGCTGAGTCC
MUSGIR.DNA      420      430      440      450      460      470
AACTACACTTCTCTGACTGGCAGAACTTCTGTGGCAGGAGAGCTTATGGGGCGGAGTCC
63A2-5'. SEQ      360      370      380
CAGAACCCACAGGTGAAAGCCCTGCTC
MUSGIR.DNA      480      490      500
CAGAACCCACAGGTGAAAGCACTGCTC

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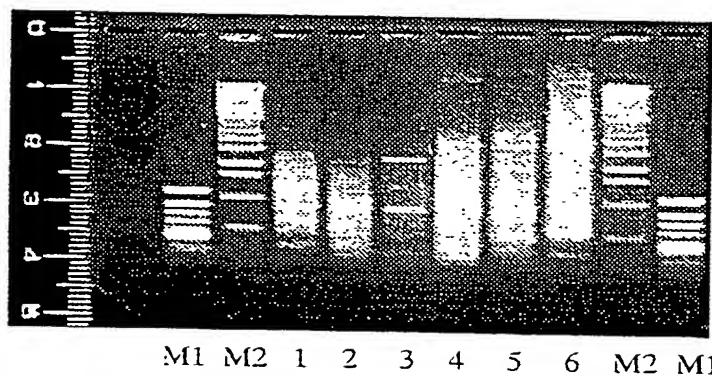
mouse CIR
Initiation codon

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OR16-F. SEQ	10	20	30	40	50	60
	TTGCCCCTCCYCATCATCTCTGTGGCCTACGCYCGTGTGGCCAARAAACTGTGGCTGTGT,					
MUSGIR. DNA	CTTCCACTCTTCATTATCTCAGTGGCCTATGCTCGTGTGGCCAAGAAGCTGTGGCTCTGT,					
	1030	1040	1050	1060	1070	1080
	70	80	90	100	110	
OR16-F. SEQ	AATATGATTGGCGATGTGACCACAGAGCAGTACTTTG-CCTKCGGCGCAAAAAGAAGAAG					
MUSGIR. DNA	AACACCATTGGCGACGTGACCACAGAGCAGTACCTCGCCCTGCGACGCAAGAAGAAGACC					
	1090	1100	1110	1120	1130	1140
	120	130	140	150	160	170
OR16-F. SEQ	ACCATCAAGATGTTGATGCTGGTGGTAGTCCCCTTTGCCCTCCGCTGGTTCCCCCTCAAC					
MUSGIR. DNA	ACCGTGAAGATGCTGGTGCTTGTGGTAGTCCTCTTTGCCCTCTGCTGGTTCCCTCTCAAC					
	1150	1160	1170	1180	1190	1200
	180	190	200	210		
OR16-F. SEQ	TGCTACGTCTCTCCTCTGTCCAGCAAGGTCATCCGC					
MUSGIR. DNA	TGCTATGTCCTCCTCTTGTCCAGCAAGGCCATCCAC					
	1210	1220	1230	1240		



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M1 ; ϕ X174 / HincII

M2 ; λ / StyI

lane 1 ; 63U ~ Anchor Primer

lane 2 ; 63-6 ~ Anchor Primer

lane 3 ; 63-7 ~ Anchor Primer

lane 4 ; 63-6 ~ Anchor Primer

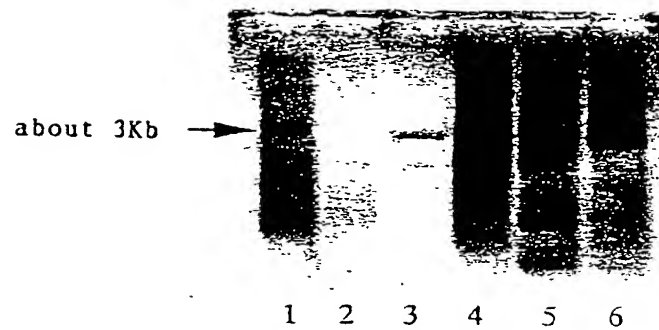
lane 5 ; 63-7 ~ Anchor Primer

lane 6 ; 63-8 ~ Anchor Primer

Primary PCR

Secondary PCR

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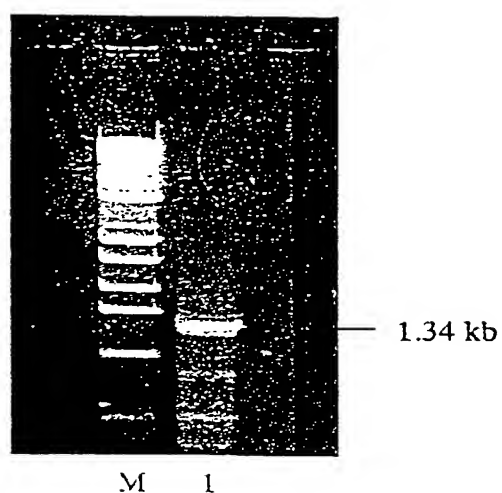


lane 1 ; 63U~Anchor Primer	Primary PCR
lane 2 ; 63-6~Anchor Primer	
lane 3 ; 63-7~Anchor Primer	
lane 4 ; 63-6~Anchor Primer	Secondary PCR
lane 5 ; 63-7~Anchor Primer	
lane 6 ; 63-8~Anchor Primer	

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63A2-3'. seq	10	20	30	40	50	60
	CCCTCTGCTGGTTCC	CCCTCAACTGCTAC	GTCTCCTCCTCTG	TCCAGCAAGGTCAT	CCGCA	
MUSGIR. DNA	1190	1200	1210	1220	1230	1240
63A2-3'. seq	70	80	90	100	110	120
	CCAACAATGCCCTCT	ACTTTGCCTTCCACT	GGTTTGCCATGAGC	AGCACCTGCTATA	AACC	
MUSGIR. DNA	1250	1260	1270	1280	1290	1300
63A2-3'. seq	130	140	150	160	170	180
	CCTTCATATACTGCT	GGCTGAACGAGAACT	TCAGGATTGAGCTAA	AGGCATTACTGAGCA		
MUSGIR. DNA	1310	1320	1330	1340	1350	1360
63A2-3'. seq	190	200	210	220	230	240
	TGTGTCAAAGACCTCC	CAAGCCTCAGGAGGAC	AGGCCACCCTCCCCAG	TTCCCTTCCTTCA		
MUSGIR. DNA	1370	1380	1390	1400	1410	1420
63A2-3'. seq	250	260	270	280	290	300
	GGGTGGCCTGGACAG	AAGAATGATGGCCAG	AGGGCTCCCTTGCCA	ATAACCTCCTGC		
MUSGIR. DNA	1430	1440	1450	1460	1470	1480
63A2-3'. seq	310	320	330	340	350	360
	CCACCTCCCAACTCC	AGTCTGGGAAGACAG	ACCTGTCATCTGTG	GGAACCCATTGTG	ACGA	
MUSGIR. DNA	1490	1500	1510	1520	1530	1540
63A2-3'. seq	370	380	390	400	410	
	TGAGT	<u>TAAAGAGGTTGGGAAGAGGGAGTGGGAGGGTCTGT</u>	CTC-CAC-CTGAGGCAG			
MUSGIR. DNA	1550	1560	1570	1580	1590	1600
mouse CIR stop codon	420	430	440	450	460	470
63A2-3'. seq	GGA--AAGAGAG-CCT	ATTCTCACACATGATC-TTCAGAGT	GTGGA	AAACACACTCCTGC		
MUSGIR. DNA	1610	1620	1630	1640	1650	1660
63A2-3'. seq	480	490				
	AGAAGCTGTAGGACTCTTGAAT					
MUSGIR. DNA	1670	1680				
	TGTCCAGCCCCATCTGATTTGC					

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M ; λ / StyI
lane 1 ; Whole Brain

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5' ATG GTC CCT CAC CTC TTG CTG CTC TGT CTC CTC CCC TTG GTG CGA GCC ACC GAG
Met Val Pro His Leu Leu Leu Leu Cys Leu Leu Pro Leu Val Arg Ala Thr Glu

CCC CAC GAG GGC CGG GCC GAC GAG CAG AGC GCG GAG GCG GCC CTG GCC GTG CCC
Pro His Glu Gly Arg Ala Asp Glu Gln Ser Ala Glu Ala Ala Leu Ala Val Pro

AAT GCC TCG CAC TTC TTC TCT TGG AAC AAC TAC ACC TTC TCC GAC TGG CAG AAC
Asn Ala Ser His Phe Phe Ser Trp Asn Asn Tyr Thr Phe Ser Asp Trp Gln Asn

TTT GTG GGC AGG AGG CGC TAC GGC GCT GAG TCC CAG AAC CCC ACG GTG AAA GCC
Phe Val Gly Arg Arg Arg Tyr Gly Ala Glu Ser Gln Asn Pro Thr Val Lys Ala

CTG CTC ATT GTG GCT TAC TCC TTC ATC ATT GTC TTC TCA CTC TTT GGC AAC GTC
Leu Leu Ile Val Ala Tyr Ser Phe Ile Ile Val Phe Ser Leu Phe Gly Asn Val

CTG GTC TGT CAT GTC ATC TTC AAG AAC CAG CGA ATG CAC TCG GCC ACC AGC CTC
Leu Val Cys His Val Ile Phe Lys Asn Gln Arg Met His Ser Ala Thr Ser Leu

TTC ATC GTC AAC CTG GCA GTT GCC GAC ATA ATG ATC ACG CTG CTC AAC ACC CCC
Phe Ile Val Asn Leu Ala Val Ala Asp Ile Met Ile Thr Leu Leu Asn Thr Pro

TTC ACT TTG GTT CGC TTT GTG AAC AGC ACA TGG ATA TTT GGG AAG GGC ATG TGC
Phe Thr Leu Val Arg Phe Val Asn Ser Thr Trp Ile Phe Gly Lys Gly Met Cys

CAT GTC AGC CGC TTT GCC CAG TAC TGC TCA CTG CAC GTC TCA GCA CTG ACA CTG
His Val Ser Arg Phe Ala Gln Tyr Cys Ser Leu His Val Ser Ala Leu Thr Leu

ACA GCC ATT GCG GTG GAT CGC CAC CAG GTC ATC ATG CAC CCC TTG AAA CCC CGG
Thr Ala Ile Ala Val Asp Arg His Gln Val Ile Met His Pro Leu Lys Pro Arg

ATC TCA ATC ACA AAG GGT GTC ATC TAC ATC GCT GTC ATC TGG ACC ATG GCT ACG
Ile Ser Ile Thr Lys Gly Val Ile Tyr Ile Ala Val Ile Trp Thr Met Ala Thr

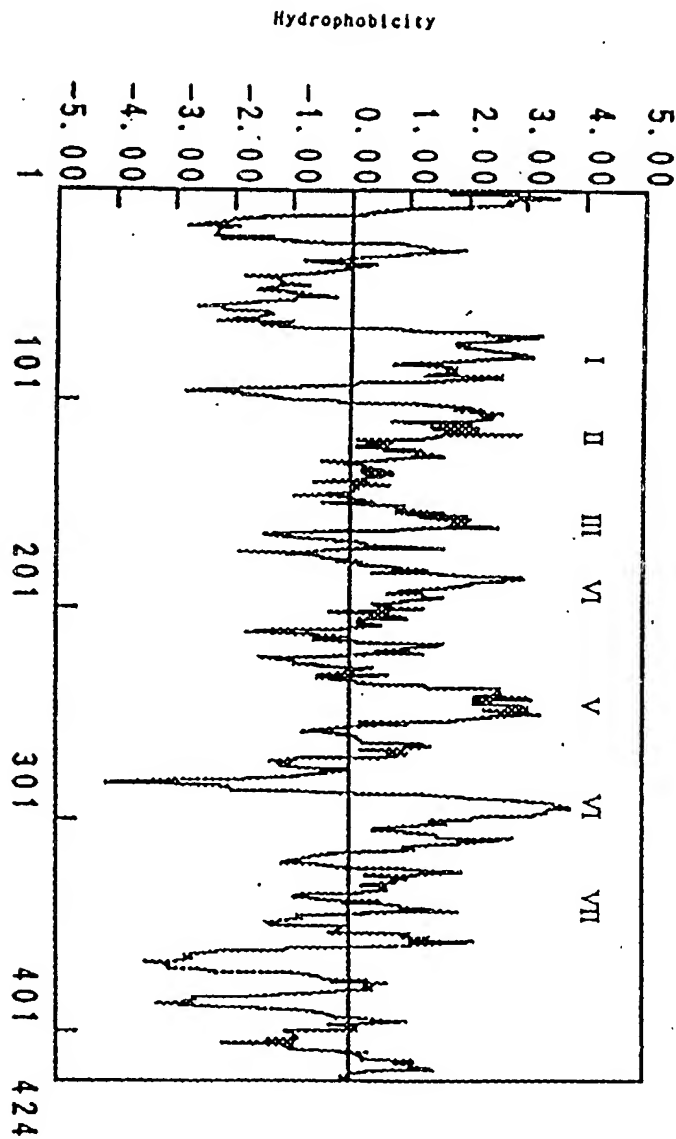
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Phe Phe Ser Leu Pro His Ala Ile Cys Gln Lys Leu Phe Thr Phe Lys Tyr Ser

GAG GAC ATT GTG CGC TCC CTC TGC CTG CCA GAC TTC CCT GAG CCA GCT GAC CTC
Glu Asp Ile Val Arg Ser Leu Cys Leu Pro Asp Phe Pro Glu Pro Ala Asp Leu

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711	720	729	738	747	756
TTC TGG AAG TAC CTG GAC TTG GCC ACC TTC ATC CTG CTC TAC ATC CTG CCC CTC					
Phe Trp Lys Tyr Leu Asp Leu Ala Thr Phe Ile Leu Leu Tyr Ile Leu Pro Leu					
765	774	783	792	801	810
CTC ATC ATC TCT GTG GCC TAC GCT CGT GTG GCC AAG AAA CTG TGG CTG TGT AAT					
Leu Ile Ile Ser Val Ala Tyr Ala Arg Val Ala Lys Lys Leu Trp Leu Cys Asn					
819	828	837	846	855	864
ATG ATT GGC GAT GTG ACC ACA GAG CAG TAC TTT GCC CTG CGG CGC AAA AAG AAG					
Met Ile Gly Asp Val Thr Thr Glu Gln Tyr Phe Ala Leu Arg Arg Lys Lys Lys					
873	882	891	900	909	918
AAG ACC ATC AAG ATG TTG ATG CTG GTG GTA GTC CTC TTT GCC CTC TGC TGG TTC					
Lys Thr Ile Lys Met Leu Met Leu Val Val Val Leu Phe Ala Leu Cys Trp Phe					
927	936	945	954	963	972
CCC CTC AAC TGC TAC GTC CTC CTC CTG TCC AGC AAG GTC ATC CGC ACC AAC AAT					
Pro Leu Asn Cys Tyr Val Leu Leu Leu Ser Ser Lys Val Ile Arg Thr Asn Asn					
981	990	999	1008	1017	1026
GCC CTC TAC TTT GCC TTC CAC TGG TTT GCC ATG AGC AGC ACC TGC TAT AAC CCC					
Ala Leu Tyr Phe Ala Phe His Trp Phe Ala Met Ser Ser Thr Cys Tyr Asn Pro					
1035	1044	1053	1062	1071	1080
TTC ATA TAC TGC TGG CTG AAC GAG AAC TTC AGG ATT GAG CTA AAG GCA TTA CTG					
Phe Ile Tyr Cys Trp Leu Asn Glu Asn Phe Arg Ile Glu Leu Lys Ala Leu Leu					
1089	1098	1107	1116	1125	1134
AGC ATG TGT CAA AGA CCT CCC AAG CCT CAG GAG GAC AGG CCA CCC TCC CCA GTT					
Ser Met Cys Gln Arg Pro Pro Lys Pro Gln Glu Asp Arg Pro Pro Ser Pro Val					
1143	1152	1161	1170	1179	1188
CCT TCC TTC AGG GTG GCC TGG ACA GAG AAG AAT GAT GGC CAG AGG GCT CCC CTT					
Pro Ser Phe Arg Val Ala Trp Thr Glu Lys Asn Asp Gly Gln Arg Ala Pro Leu					
1197	1206	1215	1224	1233	1242
GCC AAT AAC CTC CTG CCC ACC TCC CAA CTC CAG TCT GGG AAG ACA GAC CTG TCA					
Ala Asn Asn Leu Leu Pro Thr Ser Gln Leu Gln Ser Gly Lys Thr Asp Leu Ser					
1251	1260	1269			
TCT GTG GAA CCC ATT GTG ACG ATG AGT TAG 3'					
Ser Val Glu Pro Ile Val Thr Met Ser ***					

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63A2. AMI MUSGIR. AMI	1 1	10 10	20 20	30 30	40 40	50 50
	1 1	10 10	20 20	30 30	40 40	50 50
	1 1	10 10	20 20	30 30	40 40	50 50
63A2. AMI MUSGIR. AMI	51 51	60 60	70 70	80 80	90 90	100 100
	51 51	60 60	70 70	80 80	90 90	100 100
63A2. AMI MUSGIR. AMI	101 101	110 110	120 120	130 130	140 140	150 150
	101 101	110 110	120 120	130 130	140 140	150 150
63A2. AMI MUSGIR. AMI	151 151	160 160	170 170	180 180	190 190	200 200
	151 151	160 160	170 170	180 180	190 190	200 200
63A2. AMI MUSGIR. AMI	201 201	210 210	220 220	230 230	240 240	250 250
	201 201	210 210	220 220	230 230	240 240	250 250
63A2. AMI MUSGIR. AMI	251 251	260 260	270 270	280 280	290 290	300 300
	251 251	260 260	270 270	280 280	290 290	300 300
63A2. AMI MUSGIR. AMI	301 301	310 310	320 320	330 330	340 340	350 350
	301 301	310 310	320 320	330 330	340 340	350 350
63A2. AMI MUSGIR. AMI	351 351	360 360	370 370	380 380	390 390	400 400
	351 351	360 360	370 370	380 380	390 390	400 400
63A2. AMI MUSGIR. AMI	401 401	410 410	420 420	430 430	440 440	450 450
	401 401	410 410	420 420	430 430	440 440	450 450